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piece 1, NC_000913, mdtH_rimJ+, config: linear, direction: +, begin: 1124520, end: 1124804

Sequence alignment of 1124520, 1124530, 1124540, 1124550, 1124560, 1124570, 1124580, 1124590, and 1124600. The alignment shows a highly conserved sequence with a few mutations. A red dot at position 1124570 indicates a mutation from a methionine (Met) codon to a stop codon (TAA).

NC_000913.mdtH

|-----| p35-p10 1124630 total 7.0 bits

```
... sd-(7)-ir 1124684 Gap  
... sd-ir 1124684 mdtH_rimJ+  
... p35-(24)-p10 1124690 Gap  
... p35-p10 1124690 total 4.4
```

This figure displays the secondary structure of the *mdtH_rimJ+* gene. The structure is composed of various RNA elements, including hairpins and loops, color-coded in red, green, blue, and purple. Three predicted binding sites are indicated by dashed lines connecting the RNA structure to protein domains:

- p35**: Located in a purple domain, spanning approximately 3.8 bits.
- p10**: Located in a cyan domain, spanning approximately 5.9 bits.
- p10'**: Located in a red domain, spanning approximately 3.6 bits.

The sequence below the structure shows the amino acid translation of the gene, starting with fMet. Several stop codons (red dots) are present, indicating potential cleavage sites or regulatory elements.

```
... ---} sd-(7)-ir 1124684 Gap 3.7 bits
... | sd-ir 1124684 mdtH_rimJ+ total 7.7 bits
... -----} p35-(24)-p10 1124690 Gap 2.4 bits
... |----- p35-p10 1124690 total 4.4 bits
```

-----| p35-p10 1124733 total 7.2 bits

5' * *1124770 * *1124780 * *1124790 * *1124800 3'

- - - - - fMet - phe - gly - tyr - arg - ser -

- arg - glu - gly - val - gly - ile - glu - cys - leu - ala - ile - ala - val -

[... NC_000913.rimJ